

WO 00/09557 A1

---

Job No.: 1505-80958

Translated from Japanese by the Ralph McElroy Translation Company  
910 West Avenue, Austin, Texas 78701 USA

INTERNATIONAL PATENT OFFICE  
WORLD ORGANIZATION FOR INTELLECTUAL PROPERTY

International patent published on  
the basis of the Patent Cooperation Treaty  
INTERNATIONAL PUBLICATION NO. WO 00/09557 A1

International Patent Classification <sup>6</sup> :	C 07 K	14/47
	C 12 N	15/12
		//5/10
	C 12 P	21/02
	(C 12 P	21/02
	C 12 R	1:91)
International Filing No.:	PCT/JP99/04352	
International Filing Date:	August 11, 1999	
International Publication Date:	February 24, 2000	
Priority		
Date:	August 12, 1998	
Country:	JP	
No.:	Hei 10[1998]-227723	
Designated States:	AU, CA, CN, KR, US, European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE)	

NOVEL GENE AND PGTH PROTEIN ENCODED THEREBY

Inventors and	
Inventors/Applicants (only for US):	Osamu Ohara; Takahiro Nagase; Nobuo Nomura Kazusa DNA Research Institute Foundation 1532-3 Yakuni, Kisarazu-shi, Chiba-ken (JP)

Kiyoshi Takayama  
Hitoshi Toyoda;  
Makoto Yoshimoto  
Taisho Pharmaceutical Co., Ltd.  
3-24-1 Takata, Toshima-ku,  
Tokyo-to (JP)

Applicant (for all designated  
states other than US):

Kazusa DNA Research Institute  
Foundation  
1532-3 Yakuni  
Kisarazu-shi, Chiba-ken (JP)

Taisho Pharmaceutical Co., Ltd.  
3-24-1 Takata, Toshima-ku,  
Tokyo-to (JP)

Agent:

Tomizo Kitagawa  
Taisho Seiyaku K.K.  
3-24-1 Takata, Toshima-ku,  
Tokyo-to (JP)

Published  
With International Search Report.

## FOR INFORMATION ONLY

Codes for the identification of PCT contract states on the cover sheets of the documents that publish the international applications in accordance with the PCT.

AE	United Arab Emirates	KP	Democratic People's	YU	Yugoslavia
AL	Albania		Republic of Korea	ZA	South Africa
AM	Armenia	KR	South Korea	ZW	Zimbabwe
AT	Austria	KZ	Kazakhstan		
AU	Australia	LC	Saint Lucia		
AZ	Azerbaijan	LI	Liechtenstein		
BA	Bosnia-Herzegovina	LK	Sri Lanka		
BB	Barbados	LR	Liberia		
BE	Belgium	LS	Lesotho		
BF	Burkina Faso	LT	Lithuania		
BG	Bulgaria	LU	Luxembourg		
BJ	Benin	LV	Latvia		
BR	Brazil	MA	Morocco		
BY	Belarus	MC	Monaco		
CA	Canada	MD	Republic of Moldavia		
CF	Central African	MG	Madagascar		
	Republic	MK	Macedonia (former		
CG	Congo		Yugoslavian Republic		
CH	Switzerland		of Macedonia)		
CI	Côte d'Ivoire	ML	Mali		
CM	Cameroon	MN	Mongolia		
CN	China	MR	Mauritania		
CR	Costa Rica	MW	Malawi		
CU	Cuba	MX	Mexico		
CY	Cyprus	NE	Niger		
CZ	Czech Republic	NL	Netherlands		
DE	Germany	NO	Norway		
DK	Denmark	NZ	New Zealand		
DM	Dominica	PL	Poland		
EE	Estonia	PT	Portugal		
ES	Spain	RO	Romania		
FI	Finland	RU	Russian Federation		
FR	France	SD	Sudan		
GA	Gabon	SE	Sweden		
GB	United Kingdom	SG	Singapore		
GD	Grenada	SI	Slovenia		
GE	Georgia	SK	Slovakia		
GH	Ghana	SL	Sierra Leone		
GM	Gambia	SN	Senegal		
GN	Guinea	SZ	Swaziland		
GR	Greece	TD	Chad		
HR	Croatia	TG	Togo		
HU	Hungary	TJ	Tajikistan		
ID	Indonesia	TM	Turkmenistan		
IE	Ireland	TR	Turkey		
IL	Israel	TT	Trinidad and Tobago		
IN	India	TZ	Tanzania		
IS	Iceland	UA	Ukraine		
IT	Italy	UG	Uganda		
JP	Japan	US	United States of		
KE	Kenya		America		
KG	Kyrgyzstan	UZ	Uzbekistan		
		VN	Vietnam		

## Field of the technology

This invention pertains to a novel PGTH protein of human brain origin having a prostaglandin transport activity and the pgth gene encoding the protein.

## Prior art

Prostaglandin is a generic name for a series of physiologically active lipids such as prostaglandin E, prostaglandin D, prostaglandin F, prostaglandin I, prostaglandin J, etc. Prostaglandin is a physiologically active substance inside the body strongly related to control of physiological functions such as blood flow rate, sleeping, gastric mucosa protective action, thrombus formation, pregnancy, etc., through specific cell membrane or intranuclear receptors.

Prostaglandin is produced inside cells as a result of eicosapolyenic acids such as arachidonic acid, etc., being cut out by phospholipase A2 from the cell membrane and converted with cyclooxygenase and various prostaglandin synthetic enzymes by responding to various physiological stimuli, and after being released outside the cells, it has autocrine or paracrine effects. On the other hand, liberated prostaglandin is also circulated in the blood flow, taken up by a specific cell, metabolized and so disappears.

A trace amount of prostaglandin shows a strong physiological activity, and consequently, the production of prostaglandin compounds is strictly controlled by controlling the activity of production-related and metabolism-related enzymes.

However, prostaglandin has been reported to be unable to pass through the lipid double layer of the cell membrane by itself. Therefore, as a prostaglandin transport mechanism, the presence of a special protein has been presumed in the process of prostaglandin produced inside a cell exiting it and the process of prostaglandin circulating in the blood flow being taken up into a specific cell.

As a protein involved in the transport mechanism described above, prostaglandin transporter (abbreviated hPGT: human prostaglandin transporter, below) has been reported, but it is not a protein involved in the transport of all prostaglandin compounds, and there are many unclear points. Consequently, it is thought that if a biological molecule other than hPGT involved in the transport mechanism can be elucidated, the biological molecule found might be usable directly as a medical drug or indirectly as a compound for studying compounds that might be usable as a medical drug. Therefore, the objective of this invention is to identify such a molecule and use it as a medical drug or for the development of medical drugs.

### Presentation of the invention

The inventors of this invention studied diligently to find the desired protein by using genes expressed in the human brain, and as a result, they found the presence of a novel PGTH protein (prostaglandin transporter homologue), successfully isolated a pgth gene encoding the protein, and they arrived at this invention.

Specifically, this invention pertains to (a) a protein having the amino acid sequence described in sequence No. 1 or (b) a protein having an amino acid sequence with 1 to several amino acids deleted, substituted or added to the amino acid sequence of sequence No. 1, and having a prostaglandin transport activity.

Furthermore, this invention also pertains to (c) a gene comprising DNA described sequence No. 2 or (d) DNA which can be hybridized with the DNA of sequence No. 2 under stringent conditions and which encodes a protein having a prostaglandin transport activity.

The pgth gene of this invention can be isolated as a cDNA fragment containing the gene from a cDNA library of human brain origin. The cDNA library used by the inventors of this invention was prepared based on commercially available mRNA of human brain origin from the Clontech Co.

As a method for identifying the cDNA encoding a protein having a prostaglandin transport activity in the cDNA library described above, the method of Ohara, et al., (DNA Research 4: p 53, 1997) was used as an extensive cDNA library analysis method using a long-chain cDNA library. From a long-chain cDNA library of human brain origin prepared by the method of Ohara, et al., 25,000 recombinants are randomly selected, the 5' and 3' - base sequences of the cDNA from 15,000 clones were determined, and a clone showing homology to the gene encoding hPGT already reported from the 5' sequences of all the clones can be found by using a DNA analysis program (BLAST and FastA).

The presence of a region encoding the protein (ORF: open reading frame) in the base sequence can be confirmed by a conventional method using a computer program. After becoming confident of the presence of the desired gene in the cDNA sequence, the inventors of this invention found one ORF in the sequence by utilizing a computer, the gene was named pgth, and the protein encoded by the gene was named PGTH. The PGTH of the invention is a protein comprising a total of 709 amino acid residues and having a molecular weight of about 80 kd.

The invention pgth is a gene comprising 2130 bp shown in sequence No. 2. By using this pgth and conventional genetic recombination techniques using a suitable host vector system, it is possible to prepare a recombinant gene. As a suitable vector, there are plasmids of *E. coli* origin (such as pBR322, pUC118, etc.), of *Bacillus subtilis* origin, (such as pSH19, etc.) yeast origin plasmid (such as pUB110, pC194, etc.), bacteriophages, animal viruses such as retroviruses,

vaccinia virus, etc., etc. At the time of recombination, it is possible to add translation initiation and termination codons using suitable DNA adaptors. Furthermore, for gene expression, a suitable expression promoter is attached upstream of the gene. The promoter to be used is suitably selected depending on the host used. For example, if the host is *E. coli*, there are T7, lac, trp,  $\lambda$ PL promoters, etc.; if the host is a *Bacillus*, there are SPO promoters, etc.; if the host is a yeast, there are PHO5, GAP, ADH promoters, etc.; and if the host is an animal cell, there are SV40-origin, retrovirus promoters, etc.

Furthermore, the gene may be expressed as a fused protein with another protein (such as glutathione-S-transferase, protein A, etc.). In the case of a fused PGTH prepared by using such a method, a suitable protease (such as thrombin, etc.), may be used to cut out the protein.

As a host usable in the case of PGTH expression, there are various strains of *Escherichia coli*, various strains of *Bacillus subtilis*, various strains of the yeast *Saccharomyces cerevisiae* and animal cells such as COS-7, CHO cells, etc.

As a method for transforming a host cell using the above recombinant vector, a specific method conventionally used to transform the selected host cell is used.

Incidentally, in this invention, DNA which has a DNA sequence other than that shown in sequence No. 2 which can be hybridized with the DNA and encodes a protein having a prostaglandin transport activity, is also included in the scope of this invention.

Specifically, DNA which has a DNA sequence, the total length of the pgth sequence, partially changed due to various artificial treatments such as random mutations, introduction of site-specific mutations, or mutagen treatment, DNA fragment mutation, deletion ligation after scission with restriction enzymes, is also included in the scope of this invention in spite of having a DNA sequence different from that of sequence No. 2 as long as such a DNA variant can be hybridized with pgth under stringent conditions and encodes a protein having a prostaglandin transport activity.

The extent of the above DNA mutation is within the allowable range if the variant has 90% or higher homology with the DNA sequence of pgth. Furthermore, as an extent of hybridization with pgth, Southern hybridization with pgth may be carried out under conventional conditions, for example, in the case of probe labeling with a DIG DNA Labeling kit (Boehringer-Mannheim Cat. No. 1175033), hybridization conditions of a DIG Easy Hyb solution (Boehringer-Mannheim Cat. No. 1603558) at 32°C and washing of the membrane in a 5X SSC solution (containing 0.1% w/v SDS) at 50°C (1X SSC comprises 0.15M NaCl and 0.015M sodium citrate).

Furthermore, a protein encoded by the gene variant which is highly homologous to pgth as described above and has a prostaglandin transport activity is also included in the scope of this invention.

Specifically, a variant having one or more amino acids deleted, substituted or added to the amino acid sequence of PGTH is included in the scope of this invention as long as this variant is a protein having a prostaglandin transport activity.

The side chains of the amino acids, which are the constituent elements of proteins are respectively different with respect to hydrophobicity, electrical charge, size, etc., but several highly conservative relationships in the meaning of practically not affecting the three-dimensional structure (it is also called the steric structure) of proteins have been known from experiences or actual physicochemical observations. For example, for substitution of amino acid residues, there are glycine (Gly) and proline (Pro), Gly and alanine (Ala) or valine (Val), leucine (Leu) and isoleucine (Ile), glutamic acid (Glu) and glutamine (Gln), aspartic acid (Asp) and asparagine (Asn), cysteine (Cys) and threonine (Thr), Thr and serine (Ser) or Ala, lysine (Lys) and arginine (Arg), etc.

Therefore, any variant protein due to substitution, insertion, deletion, etc., in the amino acid sequence of the PGTH shown in sequence No. 1 can be said to be within the scope of this invention if the variation is a variation which conserves the three-dimensional structure of the PGTH, and the protein is a protein having a prostaglandin transport activity similar to PGTH. The allowable extent of this variation is 90% or higher homology with the amino acid sequence shown in sequence No. 1.

#### Industrial application field

The abnormal expression of pgth or functional failure of PGTH is presumed to be a critical disorder because PGTH has a prostaglandin transport activity, and consequently the normal prostaglandin production mechanism of the body is lost.

Therefore, PGTH itself is considered to be useful as a drug, and on the other hand, pgth or PGTH may be used for effectively studying or evaluating a substance having the same function as that of PGTH, a substance promoting or inhibiting its function, a substance promoting the expression of the gene, etc.

#### Best embodiment of the present invention

This invention is explained further in detail using application examples as follows, but this invention is certainly not limited to these application examples. Incidentally, unless specified, the experimental procedures used in the following application examples are those



described in standard experimental manuals such as Molecular Cloning, 2<sup>nd</sup> ed. (Cold Spring Harbor Laboratory Press, 1989), etc., and the operating manuals in commercially available kits, and they can be carried out under the conditions recommended for the respective commercially available products such as restriction enzymes, etc.

#### Application Example 1 Cloning of pgth

##### 1) Construction of a long chain cDNA library of human brain origin

An oligonucleotide (GACTAGTTCTAGATCGCGAGCGGCCGCCC(T)<sub>15</sub>) containing a NotI site was synthesized using a DNA synthesizer (ABI380B). It was used as a primer, and a double chain cDNA was synthesized using mRNA of human brain origin as a template and the SuperScript II reverse transcriptase kit (Gibco BRL). The ligation of the synthetic DNA was carried out with the cDNA and SalI site-containing adapter (Takara Shuzo), subsequently, NotI digestion was carried out, and cDNA fragments of 3 kb or larger were purified using electrophoresis with a 1% concentration of low-melting agarose.

After ligation of the purified cDNA fragments with a SalI-NotI restriction enzyme-treated pBluescriptIISK+ plasmid, the recombinant plasmids were introduced into *E. coli* ElectroMax DH10B strain (Gibco BRL) using the electroporation method. Subsequently, 25,000 recombinants were randomly selected from the library, the recombinant DNAs were extracted, and the 5'- and 3'-base sequences of the cDNAs of 15,000 clones were determined. For the sequence determination, a PE Applied Biosystem Co., DNA sequencer (ABI PRISM377) and the reaction kit from the same company were used.

##### 2) Selection of clones containing the pgth sequence

The 5 sequences of all the clones determined in 1) were compared with the sequence of hPGT already reported using DNA analytical programs (BLAST and FastA), and as a result, a clone named HK07457 showed significant homology.

##### 3) DNA fragment base sequence determination

The base sequence determination was carried out using a PE Applied Biosystem Co. DNA sequencer and the dye primer method. The sequence was mostly determined using the shotgun method, and for a portion of the base sequence, an oligonucleotide was synthesized based on the base sequence already determined, and the primer walking method was used to determine the entire base sequences of the two chains. The entire base sequence of the cDNA of the clone is shown in sequence No. 3.

The cDNA contains an ORF encoding a protein (PGTH) comprising 709 residues. A termination codon was found to appear in the upstream region of a methionine residue, which was an initiation codon of the protein, with the same reading frame. Therefore, the amino acid sequence shown in sequence No. 3 was confirmed to be the only possibility as an amino acid sequence of the protein encoded by the cDNA fragment.

Figure 1 shows the amino acid homology between already reported hPGT and the PGTH of this invention. The two show high homology, especially, the position of the cysteine residue present at the C-terminal of PGTH is preserved, and the 77<sup>th</sup> residue glutamine, 561<sup>st</sup> residue arginine and 614<sup>th</sup> residue lysine of hPGT, which are amino acids especially important for the transport activity, are also preserved in PGTH.

### Application Example 2

Confirmation of protein expression by in vitro translation of pgth

The plasmid containing pgth prepared in Application Example 1 was treated with RNase A, subsequently, RNase A was removed using ADVAMAX beads (AGTC Co.), and in vitro translation was carried out using a TNT T7 coupled reticulocyte lysate system (Promega Co.) in the presence of (<sup>35</sup>S)-methionine. A portion of the reaction mixture was separated by SDS-polyacrylamide gel electrophoresis (SDS-PAGE), and the analysis carried out using BAS-2000 (Fuji Shashin Kogyo). As a result, the presence of a single band at about 80 kd was confirmed as shown in Figure 2.

### Application Example 3

Construction of animal cell expression vector

#### 1) Amplification of ORF-containing cDNA

An oligonucleotide (following sequence 1) having a sequence upstream from the initiation codon of the protein of sequence No. 3 and oligonucleotide (following sequence 2) having a sequence of a portion downstream from the termination codon of the protein and the reverse complementary strand chain were synthesized using a DNA synthesizer (ABI Co., Model 380B).

Sequence 1

5-CTGGAGCTCACTGCACTCCAGCAGTC-3

Sequence 2

5-AGCTCACACTCGGGAATCCTCTGGCTTC-3

The recombinant cDNA containing sequence No. 3 isolated in application example 1 was used as a template, the oligonucleotides of the sequences 1 and sequences 2 were used as a primer, and the following PCR procedures were carried out using a Takara LA PCR kit Ver. 2 and the PCR thermal cycler MP (Takara Shuzo).

cDNA	5 $\mu$ L (10 ng)
10X PCR buffer (containing 25 mM Mg <sup>++</sup> )	5 $\mu$ L
2.5 mM dNTP	8 $\mu$ L
10 $\mu$ M Sequence 1	2 $\mu$ L
10 $\mu$ M Sequence 2	2 $\mu$ L
Water	27.5 $\mu$ L
LA Taq polymerase	0.5 $\mu$ L
Total amount	50 $\mu$ L

The PCR cycle was carried out by holding at 94°C for 2 mn, carrying out the reaction at 98°C for 20 sec, cooling to 68°C at a rate of 1°C/2 sec, holding at 68°C for 3 min, at 72°C for 10 min, and repeating 30 times.

The above method was used to amplify a DNA fragment (about 2.2 kb) having a portion of sequence No. 3.

## 2) Subcloning to an animal cell expression vector

The DNA fragment amplified in 1) was fractionated by 1% agarose gel electrophoresis. After staining the gel with ethidium bromide, the gel containing the desired band observed under ultraviolet irradiation was cut out. The extraction of the DNA fragment from the agarose gel and purification were carried out using a GENECLEAN II Kit (Bio101 Co.)

The extracted and purified DNA fragment was subcloned to animal cell expression vector pTARGET (Promega Co.) The ligation solution used was a Takara Ligation Kit Ver. 2 (Takara Shuzo), and the reaction was carried out with the following composition at 16°C for 1.5 h.

Extracted and purified DNA fragment	1 $\mu$ L (50 ng)
PTARGET	1 $\mu$ L (10 ng)
Water	3 $\mu$ L
<u>Ligation solution</u>	<u>5 <math>\mu</math>L</u>
Total	10 $\mu$ L

The reaction solution after the above reaction was used to transform the *E. coli* K12 strain DH5. The transformant was inoculated on an LB agar medium containing 50  $\mu$ g/mL of ampicillin (Amp), 40  $\mu$ g/mL of 5-bromo-4-chloro-3-indolyl- $\beta$ -D-galactoside (IPTG) [sic; isopropyl- $\beta$ -D-thioglucofuranoside] and 100  $\mu$ M of isopropyl- $\beta$ -D-thiogalactopyranoside

(X-gal) [sic; 5-bromo-4-chloro-3-indolyl- $\beta$ -D-galactopyranoside] \* and cultivated overnight at 37°C.

Each colony that developed on the above plate was inoculated in 10 mL of an LB liquid medium containing 50  $\mu$ g/mL of Amp, cultivation was carried out overnight at 37°C, the biomass was collected by centrifugation, and subsequently the recombinant DNA was purified using a QIAprep Spin Plasmid Miniprep Kit (Qiagen Co.) to obtain pTARGETpgth.

### 3) Determination of the base sequence of the inserted cDNA

The base sequence determination was carried out using a DNA sequencer (ABI Co., Model PRISM377) and the dye terminator method, and the whole base sequence of the two chains was determined using the primer walking method. The clone was found to contain all of the region between sequences 1 and 2 among sequence No. 3 confirming that the desired gene pTARGETpgth had been cloned.

### Application Example 4

#### Insertion into CHOk1 cells and stable transformant preparation

The recombinant DNA, pTARGETpgth, prepared in Application Example 2 has a CMV promoter upstream of pgth, and if it is inserted into an animal cell, the expression of pgth is possible.

CHOk1 cells were cultured in 60 mm diameter plastic Petri dishes. As the culture medium, Ham F-12 (Gibco, called growth medium, below) containing 10% fetal bovine serum (Dainippon Seiyaku), 50 U/mL of penicillin and 50  $\mu$ g/mL of streptomycin was used, and culture was carried out at 37°C in the presence of 5% CO<sub>2</sub>. When the cell density was 50%, LIPOFECTAMINE reagent (Gibco) containing pTARGETpgth prepared in Application Example 2 was added in a layer over the cells, incubated for 6 h, and, after replacement with the growth medium, culture was continued for 48 h. After dispersing the cells with trypsin, the cell suspension was placed in a 60 mm diameter plastic Petri dish, and culture was carried out for 24 h. After removing the culture medium, it was replaced by growth medium containing G418 (Gibco, final concentration of 500  $\mu$ g/mL). The G418 medium was changed every 3 days and culture continued for 2 weeks. When the cell colonies were observable with the naked eye, 3 colonies were isolated using stainless steel cups. As a control, only the pTARGET vector (Promega Co.) was inserted into CHOk1 cells by carrying out the same procedures as those described above to isolate a stable transformant.

---

\* [Editor's note: The compound names and abbreviations are so garbled in the original text that it is impossible to be certain whether it should be 40  $\mu$ g/mL IPTG and 100  $\mu$ m X-gal, or vice-versa.]

washed with a suitable buffer solution containing bovine serum albumin, and culture was continued for 20 min using a buffer solution containing ( $^3\text{H}$ )-labeled PGE<sub>2</sub> (Amersham Co.). After washing the cells, they were recovered, and the radioactivity taken up was measured. As a result, the prostaglandin transport activity of the CHO<sub>k</sub>1 cells with pgth inserted was statistically significantly higher than that of the CHO<sub>k</sub>1 cells with only the control vector inserted.

#### Application Example 6

Expression of pgth mRNA in human macrophages loaded with oxidized LDL

##### 1) Preparation of human macrophages loaded with oxidized LDL and normal monocyte cDNA

Normal monocyte cDNA was prepared using RNA prepared with Trizol (Gibco BRL Co.) from CD14-positive monocytes from human peripheral blood as a template and the SuperScript II reverse transcriptase kit (Gibco BRL). Human macrophages loaded with oxidized LDL were prepared by culturing normal monocytes in a RPMI-1640 medium (Dainippon Seiyaku) containing 20% AB serum and antibiotics for 14 days, adding human LDL oxidized with copper sulfate using conventional procedures (oxidized LDL) in the final concentration of 40  $\mu\text{mL}$  [sic; dimension incorrect] and continuing culture for 24 h. A method similar to that used for normal monocytes was used to prepare cDNA.

##### 2) Confirmation of pgth mRNA expression by the RT-PCR method

Oligonucleotides (following sequence 3) having a sequence contained in sequence No. 2 and oligonucleotides (following sequence 4) having the sequence of the reverse complementary strand were respectively synthesized using a DNA synthesizer (ABI Co., Model 380B).

##### Sequence 3

5-GCTCCTGCCCATTGGACGGCTTTAACC-3

##### Sequence 4

5-TCACACTCGGGAATCCTCTGGCTTC-3

The cDNA prepared in (1) was used as a template, the oligonucleotides with sequences 3 and 4 were used as primers, and the following PCR procedures were carried out using a Takara LA PCR kit Ver. 2 and the PCR thermal cycler MP (Takara Shuzo).

cDNA	2 $\mu\text{L}$ (40 ng)
10X PCR buffer (containing 25 mM $\text{Mg}^{++}$ )	1.5 $\mu\text{L}$
2.5 mM dNTP	2.4 $\mu\text{L}$

10 $\mu$ M Sequence 3	0.4 $\mu$ L
10 $\mu$ M Sequence 4	0.4 $\mu$ L
Water	10.15 $\mu$ L
LA Taq polymerase	0.15 $\mu$ L
Total amount	15 $\mu$ L

The PCR cycle was carried out by holding at 94°C for 5 min, carrying out the reaction at 94°C for 1 min, holding at 58°C for 1 min, furthermore at 72°C for 1 min, and repeating 30 times. The PCR reaction mixture was fractionated using 1% agarose gel electrophoresis. After staining the gel with ethidium bromide, the ultraviolet irradiation was carried out to detect an amplified band at about 500 bp. Similarly, the glyceraldehyde 3-phosphate dehydrogenase gene amplified primer (G3PDH, Clontech Co.) was used as the standard cDNA for PCR testing. As a result, the expression of pgth mRNA was strongly induced in the macrophages loaded with oxidized LDL, as shown in Figure 3.

Normal monocytes, macrophages loaded with oxidized LDL or equivalent cultured cells may be cultured with a test compound added, and subsequently the change in the PGTH mRNA may be measured by the method described above to screen any substance controlling PGTH mRNA expression.

#### Brief description of the figures

Figure 1 shows comparison of amino acid sequence homology between hPGT and the PGTH of this invention.

Figure 2 shows the results of SDS-PAGE of PGTH expressed using the in vitro translation method using pgth.

Figure 3 shows the results of detection of mRNA for the expression of pgth in human macrophages loaded with oxidized LDL using the RT-PCR method. In the figure o shows the results for human macrophages loaded with oxidized LDL, and m shows the results for normal human monocytes.

#### Claims

(1) A protein of the following (a) or (b).

(a) Protein comprising the amino acid sequence of sequence No. 1

(b) Protein comprising an amino acid sequence with one or more amino acids deleted, substituted or added to the amino acid sequence of sequence No. 1, and, at the same time, having a prostaglandin transport activity.



## Replacement Sheet (Regulation 26)

380	390	400	410	420	430	440
PGTH	LVVLSQVCLSSMAAGMATFLPKFLERQFSITASYANLLIGCLSPFSVIVGIVGGVLYVR----	LHLGPYCGGAL				
HPGT	LVVLAQCTFSSVIAGLSTFLNKFLEKQYGTSAAYANFLIGAVNLPAAALGMLFGGILMKRFVFSLQTIPRIATTI	400				
330	340	350	360	370	380	390
PGTH	CLLGMLLCLFFSLPLFFIGCSSHQIAGI---	THQTSAPGLELSPSCNEACSCPLDGFNPVCDPSTRVEYITPCH	510			
HPGT	ITISMILCV----	PLPFMGCSPTPTVAEVYPPSTSSSIHQ---	SPACRRDCSCPDSEIHPYVCGDNG-IEYLSPC	460	470	
410	420	430	440	450	460	470
PGTH	AGCSSVYVQDALDNSQVFTNCSCVVEGNP-VLAGSCDSTCSHLVVPFLLLVSLGSALACLTHTPTPSFNLILRGVX					
HPGT	AGCSNINMSSAT-SKQLIYLNCSCVTGGSASAKTGCSPVPCAHELLPAIFLISFVSLIACISHNPLYMMVLA	520	530	540	550	560
480	490	500	510	520	530	540
PGTH	KEDKTLAVGIQFMFLRILANWSPVIHGS	AIDTTCVHWALSC-GRRAVCRYNNDLRLNRFIGLQFFFKTGSVI-				
HPGT	QEEKSEFAGVQFLLMRLLANLPSPALYGLTI	DHSCIRWNSLCLGRRGACAYYDNDALDRDRLVGLQMGYKALGMLL	610	620	630	640
550	560	570	580	590	600	610
PGTH	-CFALVLA	VLRRQDK	KEARTKESRSPAVEQLLYSGPGKKPEDSRV			
HPGT	LCFIS	WRVYKXNK	EYNYQKAAGLI			
670	680	690	700	710	720	730
PGTH	LCFIS	WRVYKXNK	EYNYQKAAGLI			
HPGT	LCFIS	WRVYKXNK	EYNYQKAAGLI			

Figure 1 (cont.)



## Replacement Sheet (Regulation 26)

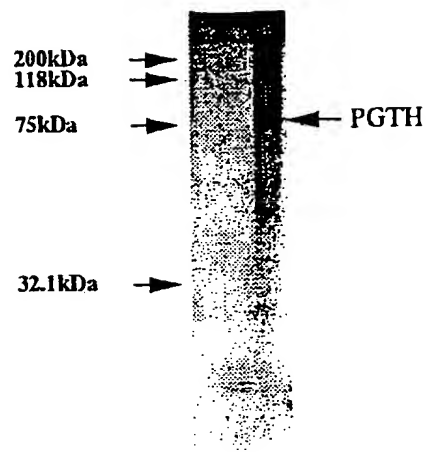


Figure 2

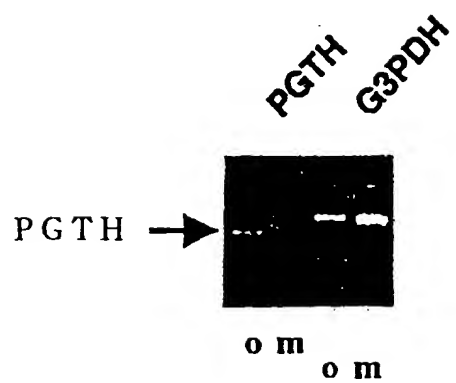


Figure 3

## S E Q U E N C E   L I S T I N G

&lt;110&gt; TAISHO PHARMACEUTICAL CO., Ltd.

&lt;120&gt; Prostaglandin

&lt;130&gt; P487

&lt;150&gt; JP10-227723

&lt;151&gt; 1998-08-12

&lt;160&gt; 3

&lt;210&gt; 1

&lt;211&gt; 709

&lt;212&gt; PRT

&lt;213&gt; Homo sapience

&lt;400&gt; 1

Met	Gly	Pro	Arg	Ile	Gly	Pro	Ala	Gly	Glu	Val	Pro	Gln	Val	Pro	5	10	15
Asp	Lys	Glu	Thr	Lys	Ala	Thr	Met	Gly	Thr	Glu	Asn	Thr	Pro	Gly	20	25	30
Gly	Lys	Ala	Ser	Pro	Asp	Pro	Gln	Asp	Val	Arg	Pro	Ser	Val	Phe	35	40	45
His	Asn	Ile	Lys	Leu	Phe	Val	Leu	Cys	His	Ser	Leu	Leu	Gln	Leu	50	55	60
Ala	Gln	Leu	Met	Ile	Ser	Gly	Tyr	Leu	Lys	Ser	Ser	Ile	Ser	Thr	65	70	75
Val	Glu	Lys	Arg	Phe	Gly	Leu	Ser	Ser	Gln	Thr	Ser	Gly	Leu	Leu	80	85	90
Ala	Ser	Phe	Asn	Glu	Val	Gly	Asn	Thr	Ala	Leu	Ile	Val	Phe	Val	95	100	105
Ser	Tyr	Phe	Gly	Ser	Arg	Val	His	Arg	Pro	Arg	Met	Ile	Gly	Tyr	110	115	120
Gly	Ala	Ile	Leu	Val	Ala	Leu	Ala	Gly	Leu	Leu	Met	Thr	Leu	Pro	125	130	135
His	Phe	Ile	Ser	Glu	Pro	Tyr	Arg	Tyr	Asp	Asn	Thr	Ser	Pro	Glu	140	145	150
Asp	Met	Pro	Gln	Asp	Phe	Lys	Ala	Ser	Leu	Cys	Leu	Pro	Thr	Thr	155	160	165
Ser	Ala	Pro	Ala	Ser	Ala	Pro	Ser	Asn	Gly	Asn	Cys	Ser	Ser	Tyr	170	175	180
Thr	Glu	Thr	Gln	His	Leu	Ser	Val	Val	Gly	Ile	Met	Phe	Val	Ala	185	190	195

Gln Thr Leu Leu Gly Val Gly Gly Val	Pro Ile Gln Pro Phe Gly	200	205	210
Ile Ser Tyr Ile Asp Asp Phe Ala His	Asn Ser Asn Ser Pro Leu	215	220	225
Tyr Leu Gly Ile Leu Phe Ala Val Thr	Met Met Gly Pro Gly Leu	230	235	240
Ala Phe Gly Leu Gly Ser Leu Met Leu	Arg Leu Tyr Val Asp Ile	245	250	255
Asn Gln Met Pro Glu Gly Gly Ile Ser	Leu Thr Ile Lys Asp Pro	260	265	270
Arg Trp Val Gly Ala Trp Trp Leu Gly	Phe Leu Ile Ala Ala Gly	275	280	285
Ala Val Ala Leu Ala Ala Ile Pro Tyr	Phe Phe Phe Pro Lys Glu	290	295	300
Met Pro Lys Glu Lys Arg Glu Leu Gln	Phe Arg Arg Lys Val Leu	305	310	315
Ala Val Thr Asp Ser Pro Ala Arg Lys	Gly Lys Asp Ser Pro Ser	320	325	330
Lys Gln Ser Pro Gly Glu Ser Thr Lys	Lys Gln Asp Gly Leu Val	335	340	345
Gln Ile Ala Pro Asn Leu Thr Val Ile	Gln Phe Ile Lys Val Phe	350	355	360
Pro Arg Val Leu Leu Gln Thr Leu Arg	His Pro Ile Phe Leu Leu	365	370	375
Val Val Leu Ser Gln Val Cys Leu Ser	Ser Met Ala Ala Gly Met	380	385	390
Ala Thr Phe Leu Pro Lys Phe Leu Glu	Arg Gln Phe Ser Ile Thr	395	400	405
Ala Ser Tyr Ala Asn Leu Leu Ile Gly	Cys Leu Ser Phe Pro Ser	410	415	420
Val Ile Val Gly Ile Val Val Gly Gly	Val Leu Val Lys Arg Leu	425	430	435
His Leu Gly Pro Val Gly Cys Gly Ala	Leu Cys Leu Leu Gly Met	440	445	450
Leu Leu Cys Leu Phe Phe Ser Leu Pro	Leu Phe Phe Ile Gly Cys	455	460	465
Ser Ser His Gln Ile Ala Gly Ile Thr	His Gln Thr Ser Ala His	470	475	480
Pro Gly Leu Glu Leu Ser Pro Ser Cys	Met Glu Ala Cys Ser Cys	485	490	495
Pro Leu Asp Gly Phe Asn Pro Val Cys	Asp Pro Ser Thr Arg Val	500	505	510
Glu Tyr Ile Thr Pro Cys His Ala Gly	Cys Ser Ser Trp Val Val	515	520	525
Gln Asp Ala Leu Asp Asn Ser Gln Val	Phe Tyr Thr Asn Cys Ser	530	535	540
Cys Val Val Glu Gly Asn Pro Val Leu	Ala Gly Ser Cys Asp Ser	545	550	555
Thr Cys Ser His Leu Val Val Pro Phe	Leu Leu Leu Val Ser Leu	560	565	570

Gly	Ser	Ala	Leu	Ala	Cys	Leu	Thr	His	Thr	Pro	Ser	Phe	Met	Leu
				575					580					585
Ile	Leu	Arg	Gly	Val	Lys	Lys	Glu	Asp	Lys	Thr	Leu	Ala	Val	Gly
				590					595					600
Ile	Gln	Phe	Met	Phe	Leu	Arg	Ile	Leu	Ala	Trp	Met	Pro	Ser	Pro
				605					610					615
Val	Ile	His	Gly	Ser	Ala	Ile	Asp	Thr	Thr	Cys	Val	His	Trp	Ala
				620					625					630
Leu	Ser	Cys	Gly	Arg	Arg	Ala	Val	Cys	Arg	Tyr	Tyr	Asn	Asn	Asp
				635					640					645
Leu	Leu	Arg	Asn	Arg	Phe	Ile	Gly	Leu	Gln	Phe	Phe	Phe	Lys	Thr
				650					655					660
Gly	Ser	Val	Ile	Cys	Phe	Ala	Leu	Val	Leu	Ala	Val	Leu	Arg	Gln
				665					670					675
Gln	Asp	Lys	Glu	Ala	Arg	Thr	Lys	Glu	Ser	Arg	Ser	Ser	Pro	Ala
				680					685					690
Val	Glu	Gln	Gln	Leu	Leu	Val	Ser	Gly	Pro	Gly	Lys	Lys	Pro	Glu
				695					700					705
Asp	Ser	Arg	Val											
				709										

<210> 2  
 <211> 2130  
 <212> DNA  
 <213> Homo sapiens

<400> 2

10	20	30	40	50	60	
aigggaccca	ggatagggcc	agcgggigag	giaccccgagg	laccagacaa	ggaaaccaa	60
gccacaalgg	gcacagaaaa	cacaccigga	ggcaaagcca	gccagaccc	icaggacgig	120
cggccaagig	igticcataa	calcaagcig	ticgticigt	gccacagcci	gcigcagcig	180
ggcgagcica	lgaicccgg	ciacclaaag	agciccatci	ccacagigga	gaagcgcttc	240
ggcctctcca	gccagacgic	ggggcigcig	gcctcctcca	acgaggiggg	gaacacagcc	300
ttgatigtgt	ttgtagctta	tttgggcagc	cgggigcacc	gaccccgaa	gatiggctat	360
ggggctalcc	ttgtggccct	ggcgggcccig	cicagacac	lccgcacit	catctcggag	420
ccataccgct	acgacaacac	cagcccgag	gatalgccac	aggacitcaa	ggctlccctg	480
tgccigccca	caaccicggc	cccagccctg	gccccctcca	aiggcaactg	cicaagctac	540
acagaaaccc	agcatcigag	tgiggigggg	atcatgttcg	tggcacagac	ccigtgggc	600

giggcgggg lgcccalica gcccllggc alclccclaca lcgatgactl lgcccaaac 660  
agcaaclegc cccclaccl cgggalccig lllgcagiga ccalgaiggg gccaggccig 720  
gcclllgggc lgggcagcc lalgclgcgc clllaiglgg acallaaacca galgccagaa 780  
ggiggialca gccigaccal aaaggacccc cgalgggtgg glgcclggig gclgggllc 840  
clcalcgclg ccggigcagl ggccciggl gccalcccc clclclclcl ccccaaggaa 900  
algcccaagg aaaaacgiga gcllcaglll cggcgaaagg lcllagcagl cacagactca 960  
cclgccagga agggcaagga clclcccccl aagcagagcc clggggaglc cacgaagaag 1020  
caggalggcc laglccagal lgcaccaaac clgacigiga lccagllcal laaagclcl 1080  
cccaggglgc lgcigcagac cclacgccac cccalcllcc lglggllgl cclglcccag 1140  
glalglclgl calccaiggg lgggggcaig gccaccllcc lgcccaagll cclggagcgc 1200  
caglllcca lcacagcccl clacgccaac clgclcalcg gclgccclcl clcccllclg 1260  
glcalclgg gcalclggll ggglggcglc clggllcaagc ggclccaccl ggcccclgig 1320  
ggalgcggig ccclllgcl gclggggaig clgcllgcc clclcllclag cclgccgcl 1380  
llclllalcl gclgclccag ccaccagall gggggcalca cacaccagac caglgccac 1440  
cclgggcig agclgclcc aagclgcal gaggccglcl cclgccccl ggacggcll 1500  
aaccclgcl ggcaccccag cclclgllg gaalacalca caccclgcca cgcaggclgc 1560  
lcaagclgg lggllccagga lgcclggac aacagccagg llclclacac caaclgcagc 1620  
lgclggllg agggcaaccc cglgclggca ggalcclgc aclcaacglc cagccalclg 1680  
lgglgccc lclgclcll gglcagccg ggclcgccc lggcclgcl caccacaca 1740  
cccclclla lglcalcll aagaggaglg aagaaagaag acaagacll ggclgtgggc 1800  
alccagllca lglclcgag gallllggcc lggalgccca gcccclgcl ccacggcagc 1860  
gccalgcaca ccaccigll gcalgggccc clgagcllg ggcglcgagc lglclgclgc 1920  
lcllacaala algacclgl cggaaaccgg llcalcggcc lccagllcl clcaaaaaca 1980  
ggllclgiga lclgcllcl clagllllg gclglclga ggcagcagga caaagaggca 2040  
aggaccaaag agagcagalc cagcccggc glagagcagc aallgclagl glcggggcca 2100

gggaagaagc cagaggatic ccgagtgiga

2130

<210> 3  
 <211> 4083  
 <212> DNA  
 <213> Homo sapiens

<400> 3

aagtgaccca gggagacaaa cacitggaga tacttggggc tgagtltgag caagactccc 60  
 taacctgtgt cttgacaagt ctgatttctt gtgtggccca agaagaactg accccgtgtc 120  
 tggagctccc accgtttatg catctctgtt gtggctcacc tgcctgtgtc tccaggagcc 180  
 ccctgagaaga ttggctctct cttctctgtt aagctccagg tcttgagatt gaattagggg 240  
 ctggagctca ctgcactcca gcagtc 266  
 atg gga ccc agg ata ggg cca gcg ggt gag gla ccc cag gla cca 311  
 Met Gly Pro Arg Ile Gly Pro Ala Gly Glu Val Pro Gln Val Pro  
 5 10 15  
 gac aag gaa acc aaa gcc aca atg ggc aca gaa aac aca cct gga 356  
 Asp Lys Glu Thr Lys Ala Thr Met Gly Thr Glu Asn Thr Pro Gly  
 20 25 30  
 ggc aaa gcc agc cca gac cct cag gac gtt cgg cca agt gtt ttc 401  
 Gly Lys Ala Ser Pro Asp Pro Gln Asp Val Arg Pro Ser Val Phe  
 35 40 45  
 cat aac atc aag ctg ttc gtt ctg tgc cac agc ctg ctg cag ctg 446  
 His Asn Ile Lys Leu Phe Val Leu Cys His Ser Leu Leu Gln Leu  
 50 55 60  
 gcg cag ctg atg atc tcc ggc tac cta aag agc tcc atc tcc aca 491  
 Ala Gln Leu Met Ile Ser Gly Tyr Leu Lys Ser Ser Ile Ser Thr  
 65 70 75  
 gtt gag aag cgt ttc ggc ctg tcc agc cag acg tgc ggg ctg ctg 536  
 Val Glu Lys Arg Phe Gly Leu Ser Ser Gln Thr Ser Gly Leu Leu  
 80 85 90  
 gcc tcc ttc aac gag gtt ggg aac aca gcc ttg att gtt ttt gtt 581  
 Ala Ser Phe Asn Glu Val Gly Asn Thr Ala Leu Ile Val Phe Val  
 95 100 105  
 agc tat ttt ggc agc cgt gtt cac cga ccc cga atg att ggc tat 626  
 Ser Tyr Phe Gly Ser Arg Val His Arg Pro Arg Met Ile Gly Tyr  
 110 115 120  
 ggg gct atc ctt gtt gcc ctg gcg ggc ctg ctg atg act ctg ccg 671  
 Gly Ala Ile Leu Val Ala Leu Ala Gly Leu Leu Met Thr Leu Pro  
 125 130 135  
 cac ttc atc tgc gag cca tac cgt tac gac aac acc agc cct gag 716  
 His Phe Ile Ser Glu Pro Tyr Arg Tyr Asp Asn Thr Ser Pro Glu  
 140 145 150

gal atg cca cag gac ttc aag gct tcc ctg tgc ctg ccc aca acc	761
Asp Met Pro Gln Asp Phe Lys Ala Ser Leu Cys Leu Pro Thr Thr	
155 160 165	
tcg gcc cca gcc tcg gcc ccc tcc aat ggc aac tgc tca agc tac	806
Ser Ala Pro Ala Ser Ala Pro Ser Asn Gly Asn Cys Ser Ser Tyr	
170 175 180	
aca gaa acc cag cat ctg agt gtg gtg ggg aic atg ttc gtg gca	851
Thr Glu Thr Gln His Leu Ser Val Val Gly Ile Met Phe Val Ala	
185 190 195	
cag acc ctg ctg ggc gtg ggc ggg gtg ccc att cag ccc ttt ggc	896
Gln Thr Leu Leu Gly Val Gly Gly Val Pro Ile Gln Pro Phe Gly	
200 205 210	
atc tcc tac atc gal gac ttt gcc cac aac agc aac tcg ccc ctg	941
Ile Ser Tyr Ile Asp Asp Phe Ala His Asn Ser Asn Ser Pro Leu	
215 220 225	
tac ctg ggg aic ctg ttt gca gtg acc atg atg ggg cca ggc ctg	986
Tyr Leu Gly Ile Leu Phe Ala Val Thr Met Met Gly Pro Gly Leu	
230 235 240	
gcc ttt ggg ctg ggc agc ctg atg ctg cgc ctt tat gtg gac att	1031
Ala Phe Gly Leu Gly Ser Leu Met Leu Arg Leu Tyr Val Asp Ile	
245 250 255	
aac cag atg cca gaa ggt ggt aic agc ctg acc ala aag gac ccc	1076
Asn Gln Met Pro Glu Gly Gly Ile Ser Leu Thr Ile Lys Asp Pro	
260 265 270	
cga tgg gtg ggt gcc tgg tgg ctg ggt ttc ctg atc gct gcc ggt	1121
Arg Trp Val Gly Ala Trp Trp Leu Gly Phe Leu Ile Ala Ala Gly	
275 280 285	
gca gtg gcc ctg gct gcc atc ccc tac ttc ttc ttc ccc aag gaa	1166
Ala Val Ala Leu Ala Ala Ile Pro Tyr Phe Phe Phe Pro Lys Glu	
290 295 300	
atg ccc aag gaa aaa cgt gag ctt cag ttt cgg cga aag gtc tta	1211
Met Pro Lys Glu Lys Arg Glu Leu Gln Phe Arg Arg Lys Val Leu	
305 310 315	
gca gtc aca gac tca cct gcc agg aag ggc aag gac tct ccc tct	1256
Ala Val Thr Asp Ser Pro Ala Arg Lys Gly Lys Asp Ser Pro Ser	
320 325 330	
aag cag agc cct ggg gag tcc acg aag aag cag gat ggc cta gtc	1301
Lys Gln Ser Pro Gly Glu Ser Thr Lys Lys Gln Asp Gly Leu Val	
335 340 345	
cag att gca cca aac ctg act gtg atc cag ttc att aaa gtc ttc	1346
Gln Ile Ala Pro Asn Leu Thr Val Ile Gln Phe Ile Lys Val Phe	
350 355 360	
ccc agg gtg ctg ctg cag acc cta cgc cac ccc atc ttc ctg ctg	1391
Pro Arg Val Leu Leu Gln Thr Leu Arg His Pro Ile Phe Leu Leu	
365 370 375	
gtg gtc ctg tcc cag gta tgc ttg tca tcc atg gct gcg ggc atg	1436
Val Val Leu Ser Gln Val Cys Leu Ser Ser Met Ala Ala Gly Met	
380 385 390	
gcc acc ttc ctg ccc aag ttc ctg gag cgc cag ttt tcc atc aca	1481
Ala Thr Phe Leu Pro Lys Phe Leu Glu Arg Gln Phe Ser Ile Thr	

395	400	405	
gcc tcc tac gcc aac ctc ctc atc gcc tgc ctc tcc ttc cct tgc			1526
Ala Ser Tyr Ala Asn Leu Leu Ile Gly Cys Leu Ser Phe Pro Ser			
410	415	420	
gtc atc gtc gcc atc gtc gtc ggt gcc gtc ctc gtc aag cgg ctc			1571
Val Ile Val Gly Ile Val Val Gly Gly Val Leu Val Lys Arg Leu			
425	430	435	
cac ctc gcc cct gtc gga tgc ggt gcc ctt tgc ctc ctc ggg atg			1616
His Leu Gly Pro Val Gly Cys Gly Ala Leu Cys Leu Leu Gly Met			
440	445	450	
ctc ctc tgc ctc ttc ttc agc ctc cgc ctc ttc ttt atc gcc tgc			1661
Leu Leu Cys Leu Phe Phe Ser Leu Pro Leu Phe Phe Ile Gly Cys			
455	460	465	
tcc agc cac cag att gcg gcc atc aca cac cag acc agt gcc cac			1706
Ser Ser His Gln Ile Ala Gly Ile Thr His Gln Thr Ser Ala His			
470	475	480	
cct ggg ctc gag ctc tct cca agc tgc atg gag gcc tgc tcc tgc			1751
Pro Gly Leu Glu Leu Ser Pro Ser Cys Met Glu Ala Cys Ser Cys			
485	490	495	
cca ttg gac gcc ttt aac cct gtc tgc gac ccc agc act cgt gtc			1796
Pro Leu Asp Gly Phe Asn Pro Val Cys Asp Pro Ser Thr Arg Val			
500	505	510	
gaa tac atc aca ccc tgc cac gca gcc tgc tca agc tgg gtc gtc			1841
Glu Tyr Ile Thr Pro Cys His Ala Gly Cys Ser Ser Trp Val Val			
515	520	525	
cag gat gct ctc gac aac agc cag gtt ttc tac acc aac tgc agc			1886
Gln Asp Ala Leu Asp Asn Ser Gln Val Phe Tyr Thr Asn Cys Ser			
530	535	540	
tgc gtc gtc gag gcc aac ccc gtc ctc gca gga tcc tgc gac tca			1931
Cys Val Val Glu Gly Asn Pro Val Leu Ala Gly Ser Cys Asp Ser			
545	550	555	
acg tgc agc cat ctc gtc gtc ccc ttc ctc ctc ctc gtc agc ctc			1976
Thr Cys Ser His Leu Val Val Pro Phe Leu Leu Leu Val Ser Leu			
560	565	570	
ggc tgc gcc ctc gcc tgc ctc acc cac aca ccc tcc ttc atg ctc			2021
Gly Ser Ala Leu Ala Cys Leu Thr His Thr Pro Ser Phe Met Leu			
575	580	585	
atc cta aga gga gtc aag aaa gaa gac aag act ttg gct gtc gcc			2066
Ile Leu Arg Gly Val Lys Lys Glu Asp Lys Thr Leu Ala Val Gly			
590	595	600	
atc cag ttc atg ttc ctc agg att ttg gcc tgg atg ccc agc ccc			2111
Ile Gln Phe Met Phe Leu Arg Ile Leu Ala Trp Met Pro Ser Pro			
605	610	615	
gtc atc cac gcc agc gcc atc gac acc acc tgc gtc cac tgg gcc			2156
Val Ile His Gly Ser Ala Ile Asp Thr Thr Cys Val His Trp Ala			
620	625	630	
ctc agc tgc ggg cgt cga gct gtc tgc ctc tac tac aat aat gac			2201
Leu Ser Cys Gly Arg Arg Ala Val Cys Arg Tyr Tyr Asn Asn Asp			
635	640	645	
ctc ctc cga aac cgg ttc atc gcc ctc cag ttc ttc ttc aaa aca			2246



Leu Leu Arg Asn Arg Phe Ile Gly Leu Gln Phe Phe Phe Lys Thr  
 650 655 660  
 ggi tct gfg atc lgc itc gcc ita gti lig gcl glc cig agg cag 2291  
 Gly Ser Val Ile Cys Phe Ala Leu Val Leu Ala Val Leu Arg Gln  
 665 670 675  
 cag gac aaa gag gca agg acc aaa gag agc aga tcc agc ccl gcc 2336  
 Gln Asp Lys Glu Ala Arg Thr Lys Glu Ser Arg Ser Ser Pro Ala  
 680 685 690  
 gla gag cag caa lig cta gfg tcc ggg cca ggg aag aag cca gag 2381  
 Val Glu Gln Gln Leu Leu Val Ser Gly Pro Gly Lys Lys Pro Glu  
 695 700 705  
 gal tcc cga gfg lga 2396  
 Asp Ser Arg Val  
 709

gcigtcttgg ggccccacct ggccaagagt agcagccaca gcaglacctc ccttgagttc 2456  
 ttigcccaag atiggggtgc aagagccctg tglccattc tggctccctc actaaatlgc 2516  
 tggltgactt caggcaagac atgaltctc tctcagccit tgcitgctag tctgaaccaa 2576  
 agagttgttt gggtatttgc tggtttggcc attcttgtag caagaggggc ttcttccctc 2636  
 ttccccagc cagccagctg tcttggggcc aggccttctt ggggtggaaag aagtatacct 2696  
 ttccctgggg ccctaggata gcaaagtag ccatagtggt ccaggttgc cctcatgctg 2756  
 ggccccagcc caggcttgc cctgcttga tcccttctt ttagccctag ccatctctt 2816  
 tccagtagga atgaacttgc cagcttctc gctcttctc ctatgacct ctgttgggtc 2876  
 aggttacct cagcttctt ccccaactc agcagccctt aagaagtgc ccttgggtc 2936  
 cccctggagg cagagcactg agcttgacct tgggttagct cccacaggga ggacggagct 2996  
 ggcttcagga gtgggacacc cagacttgc agggcttca agaggtctgt gtgggggtcc 3056  
 caggaatctt tagctgaagc ggggagactc acttccatc ttaggaaat ctagccctt 3116  
 ccttcaggga gccacgttgc aggtttaggc ccaacacctg ccttagggcc ctgggttggc 3176  
 aagcttgggc cctgggttag ggaggagac ttaggttctc acttgggtat ttcttaatt 3236  
 cagacaaaca cacactcagc gctcactc tgalcttctc acatgttcaa gattctcac 3296  
 atgttacct gggttctcaa agtcttctg accttctga ctaggacct aattcttct 3356  
 ttcttctg ggttcttggc tcttctc cttgggtcgt gtggataatg tttagtctg 3416  
 ttagactt ttgttgggtt ggttcttgt tcttctg cttgggttgt gtcaggttca 3476

ggactglagi gcigggagca gtaaagctca gcicigigia algaglgalg clalggclig 3536  
ciclgigicli algalccaal cctilicliac atcagcccll glililgilli atggclaglc 3596  
llaiclggcc lggllalilc cligcgggga ggagagggli lgclaaiclg clcccagccc 3656  
aacctallac caccacccl cgcigggacc lacigcicgg gaggcagcag acaggagacc 3716  
accagcaglg gclicclggc cciglgcigx gggigggggx aagciggggg cacaiglggc 3776  
ccligcclic lgagcagcic ccaglgccag ggclllgaga clilcccaca lgalaaaaga 3836  
aaagggaggi acagaaglic caalicccll lllalililgc lggllgglat ciglaaaigi 3896  
llaataaala tcigagcag laiclalcaa cgccaagaal licaaagici ccllcaaaa 3956  
talgaggccl ltaggalgli lataliccll calccclcll glilcccagg llllgcagg 4016  
aaaaaaaglc lggaaltala galacagccl attallaaal lgticclgc ataaaaaaa 4076  
aaaaaaa 4083

# INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP99/04352

## A. CLASSIFICATION OF SUBJECT MATTER

Int.Cl.<sup>6</sup> C07K 14/47, C12N 15/12//C12N 5/10, C12P 21/02,  
(C12P 21/02, C12R 1:91)

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)  
Int.Cl.<sup>6</sup> C07K 14/47, C12N 15/12, C12N 5/10, C12P 21/02,

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)  
SwissProt/PIR/GeneSeq, Genbank/EMBL/DDBJ/GeneSeq,  
WPI (DIALOG), BIOSIS (DIALOG)

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	US, 5792851, A (Albert Einstein College of Medicine of Yeshiva University, a Division of Yeshiva University) 11 August, 1998 (11.08.98) (Family: none)	1, 2
Y	Journal of Clinical Investigation, Vol.98, no.5 (1996) Lu Run, et al., "Cloning, in vitro expression, and tissue distribution of a human prostaglandin transporter cDNA (hPGT)" see p.1142-1149, (1996)	1, 2
Y	Biochemical and Biophysical Research Communications, Vol.246, No.3, (May 29, 1998), Lu Run, et al., "Molecular cloning of the gene for human prostaglandin transporter hPGT: Gene organization, promoter activity and chromosomal localization", see p.805-812,	1, 2

☒ Further documents are listed in the continuation of Box C.

☐ See patent family annex.

\* Special categories of cited documents:  
"A" document defining the general state of the art which is not considered to be of particular relevance  
"E" earlier document but published on or after the international filing date  
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)  
"O" document referring to an oral disclosure, use, exhibition or other means  
"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention  
"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone  
"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art  
"&" document member of the same patent family

Date of the actual completion of the international search  
09 November, 1999 (09.11.99)

Date of mailing of the international search report  
24 November, 1999 (24.11.99)

Name and mailing address of the ISA/  
Japanese Patent Office

Authorized officer

Facsimile No.

Telephone No.

## INTERNATIONAL SEARCH REPORT

International Application No.

PCT/JP99/04352

## C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	Science, vol.268, No.5212, (1995), Kanai Naoaki et al., "Identification and Characterization of a prostaglandin transporter ", see p.866-869,	1-2